

#6

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,627
Source: PCT
Date Processed by STIC: 16/26/04

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,627

DATE: 10/26/2004
TIME: 17:39:36

Input Set : A:\2923-657.txt
Output Set: N:\CRF4\10262004\J511627.raw

3 <110> APPLICANT: Eulenberg, Karsten
4 Steuernagel, Arnd
5 Haeder, Thomas
6 Meise, Martin
7 Guenter, Broenner
9 <120> TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
11 <130> FILE REFERENCE: 2923-657
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/511,627
C--> 13 <141> CURRENT FILING DATE: 2004-10-18
13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/04650
14 <151> PRIOR FILING DATE: 2003-05-02
16 <150> PRIOR APPLICATION NUMBER: EP 02 010 948.4
17 <151> PRIOR FILING DATE: 2002-05-16
19 <150> PRIOR APPLICATION NUMBER: EP 02 010 332.1
20 <151> PRIOR FILING DATE: 2002-05-07
22 <150> PRIOR APPLICATION NUMBER: EP 02 009 883.6
23 <151> PRIOR FILING DATE: 2002-05-02
25 <160> NUMBER OF SEQ ID NOS: 73
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 615
31 <212> TYPE: PRT
32 <213> ORGANISM: Drosophila melanogaster
34 <400> SEQUENCE: 1
36 Leu Val Lys Ile Ala Asn Tyr Gln Asp Leu Leu Gly Ser His His Gln
37 1 5 10 15
40 Leu Leu Ile Ala Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Glu
41 20 25 30
44 Pro Gln Leu Gln Leu Gln His Leu Leu Pro Ala Ala Pro Thr Thr Pro
45 35 40 45
48 Ala Val Ile Ser Asn Pro Ile Asn Ser Ile Gly Pro Ile Asn Gln Ile
49 50 55 60
52 Ser Ser Ser Ser His Pro Ser Asn Asn Asn Gln Gln Ala Val Phe Glu
53 65 70 75 80
56 Lys Ala Ile Thr Ile Ser Ser Ile Ala Ile Lys Arg Arg Pro Thr Leu
57 85 90 95
60 Pro Gln Thr Pro Ala Ser Ala Pro Gln Val Leu Ser Pro Ser Pro Lys
61 100 105 110
64 Arg Gln Cys Ala Ala Ala Val Ser Val Leu Pro Val Thr Val Pro Val
65 115 120 125
68 Pro Val Pro Val Ser Val Pro Leu Pro Val Ser Val Pro Val Pro Val
69 130 135 140
72 Ser Val Lys Gly His Pro Ile Ser His Thr His Gln Ile Ala His Thr

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73	145	150	155	160
76	His Gln Ile Ser His Ser His Pro Ile Ser His Pro His His His Gln			
77		165	170	175
80	Leu Ser Phe Ala His Pro Thr Gln Phe Ala Ala Ala Val Ala Ala His			
81		180	185	190
84	His Gln Gln Gln Gln Gln Gln Ala Gln Gln Gln Gln Gln Ala Val			
85		195	200	205
88	Gln Gln Gln Gln Gln Ala Val Gln Gln Gln Val Ala Tyr Ala			
89		210	215	220
92	Val Ala Ala Ser Pro Gln Leu Gln Gln Gln Gln Gln Gln His			
93		225	230	235
96	Arg Leu Ala Gln Phe Asn Gln Ala Ala Ala Ala Leu Leu Asn Gln			
97		245	250	255
100	His Leu Gln Gln His Gln Ala Gln Gln Gln His Gln Ala Gln			
101		260	265	270
104	Gln Gln Ser Leu Ala His Tyr Gly Gly Tyr Gln Leu His Arg Tyr Ala			
105		275	280	285
108	Pro Gln Gln Gln Gln His Ile Leu Leu Ser Ser Gly Ser Ser Ser			
109		290	295	300
112	Ser Lys His Asn Ser Asn Asn Ser Asn Thr Ser Ala Gly Ala Ala			
113		305	310	315
116	320			
117	Ser Ala Ala Val Pro Ile Ala Thr Ser Val Ala Ala Val Pro Thr Thr			
118		325	330	335
120	Gly Gly Ser Leu Pro Asp Ser Pro Ala His Glu Ser His Ser His Glu			
121		340	345	350
124	Ser Asn Ser Ala Thr Ala Ser Ala Pro Thr Thr Pro Ser Pro Ala Gly			
125		355	360	365
128	Ser Val Thr Ser Ala Ala Pro Thr Ala Thr Ala Thr Ala Ala Ala Ala			
129		370	375	380
132	Gly Ser Ala Ala Ala Thr Ala Ala Ala Thr Gly Thr Pro Ala Thr Ser			
133		385	390	395
136	400			
137	Ala Val Ser Asp Ser Asn Asn Asn Leu Asn Ser Ser Ser Ser Asn			
138		405	410	415
140	Ser Asn Ser Asn Ala Ile Met Glu Asn Gln Met Ala Leu Ala Pro Leu			
141		420	425	430
144	Gly Leu Ser Gln Ser Met Asp Ser Val Asn Thr Ala Ser Asn Glu Glu			
145		435	440	445
148	Glu Val Arg Thr Leu Phe Val Ser Gly Leu Pro Met Asp Ala Lys Pro			
149		450	455	460
152	Arg Glu Leu Tyr Leu Leu Phe Arg Ala Tyr Glu Gly Tyr Glu Gly Ser			
153		465	470	475
156	480			
157	Leu Leu Lys Val Thr Ser Lys Asn Gly Lys Thr Ala Ser Pro Val Gly			
158		485	490	495
160	Phe Val Thr Phe His Thr Arg Ala Gly Ala Glu Ala Ala Lys Gln Asp			
161		500	505	510
164	Leu Gln Gly Val Arg Phe Asp Pro Asp Met Pro Gln Thr Ile Arg Leu			
165		515	520	525
168	Glu Phe Ala Lys Ser Asn Thr Lys Val Ser Lys Pro Lys Pro Gln Pro			
169		530	535	540

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172 Asn Thr Ala Thr Thr Ala Ser His Pro Ala Leu Met His Pro Leu Thr
173 545 550 555 560
176 Gly His Leu Gly Gly Pro Phe Phe Pro Gly Gly Pro Glu Leu Trp His
177 565 570 575
180 His Pro Leu Ala Tyr Ser Ala Ala Ala Ala Glu Leu Pro Gly Ala
181 580 585 590
184 Ala Ala Leu Gln His Ala Thr Leu Val His Pro Ala Leu His Pro Gln
185 595 600 605
188 Val Pro Val Arg Ser Tyr Leu
189 610 615
192 <210> SEQ ID NO: 2
193 <211> LENGTH: 17
194 <212> TYPE: DNA
195 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 2
198 cctggatcgc accaacg 17
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 22
203 <212> TYPE: DNA
204 <213> ORGANISM: Mus musculus
206 <400> SEQUENCE: 3
207 ttaagctgct gttccatgac ca 22
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 20
212 <212> TYPE: DNA
213 <213> ORGANISM: Mus musculus
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (1)..(1)
219 <223> OTHER INFORMATION: FAM reporter dye
221 <220> FEATURE:
222 <221> NAME/KEY: misc_feature
223 <222> LOCATION: (20)..(20)
224 <223> OTHER INFORMATION: TAMRA quencher dye
226 <400> SEQUENCE: 4
227 tccaggctgc catagcgcgc 20
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 19
232 <212> TYPE: DNA
233 <213> ORGANISM: Mus musculus
235 <400> SEQUENCE: 5
236 cctgccaacc ctgatcaca 19
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 20
241 <212> TYPE: DNA
242 <213> ORGANISM: Mus musculus
244 <400> SEQUENCE: 6
245 tttcaatgcc agcgaaagtg 20
248 <210> SEQ ID NO: 7

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249 <211> LENGTH: 23
250 <212> TYPE: DNA
251 <213> ORGANISM: Mus musculus
254 <220> FEATURE:
255 <221> NAME/KEY: misc_feature
256 <222> LOCATION: (1)..(1)
257 <223> OTHER INFORMATION: FAM reporter dye
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
261 <222> LOCATION: (23)..(23)
262 <223> OTHER INFORMATION: TAMRA quencher dye
264 <400> SEQUENCE: 7
265 cgggtggctac agacttgcca cg 23
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 22
270 <212> TYPE: DNA
271 <213> ORGANISM: Mus musculus
273 <400> SEQUENCE: 8
274 agcggtgggt ctatgtcgat tt 22
277 <210> SEQ ID NO: 9
278 <211> LENGTH: 19
279 <212> TYPE: DNA
280 <213> ORGANISM: Mus musculus
282 <400> SEQUENCE: 9
283 cgggatttag gaaccggct 19
286 <210> SEQ ID NO: 10
287 <211> LENGTH: 22
288 <212> TYPE: DNA
289 <213> ORGANISM: Mus musculus
292 <220> FEATURE:
293 <221> NAME/KEY: misc_feature
294 <222> LOCATION: (1)..(1)
295 <223> OTHER INFORMATION: FAM reporter dye
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <222> LOCATION: (22)..(22)
300 <223> OTHER INFORMATION: TAMRA quencher dye
302 <400> SEQUENCE: 10
303 aggctgtgaag cccgtggat ct 22
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 21
308 <212> TYPE: DNA
309 <213> ORGANISM: Mus musculus
311 <400> SEQUENCE: 11
312 acaaggatgg caagagcaga g 21
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 22
317 <212> TYPE: DNA
318 <213> ORGANISM: Mus musculus
  
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Input Set : A:\2923-657.txt
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320 <400> SEQUENCE: 12
321 atggaaatttgc tt
324 <210> SEQ ID NO: 13
325 <211> LENGTH: 26
326 <212> TYPE: DNA
327 <213> ORGANISM: Mus musculus
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: (1)..(1)
333 <223> OTHER INFORMATION: FAM reporter dye
335 <220> FEATURE:
336 <221> NAME/KEY: misc_feature
337 <222> LOCATION: (26)..(26)
338 <223> OTHER INFORMATION: TAMRA quencher dye
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341 catgggcact gtcacttttg agcagg
344 <210> SEQ ID NO: 14
345 <211> LENGTH: 914
346 <212> TYPE: PRT
347 <213> ORGANISM: Drosophila melanogaster
349 <400> SEQUENCE: 14
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355 Lys Ser Leu Trp Trp His Arg Arg Thr Ser Glu Phe Ser Ile Lys Ala
356 20 25 30
359 Gly Trp Asp Leu Ser Ser Val Asp Asp Ile Glu Cys Ile Gly Val Thr
360 35 40 45
363 His Gly Ile Val Gly Val Ile Ser Leu Pro Asn Val Tyr Glu Pro His
364 50 55 60
367 Leu Val Val Val Lys Glu Ala Ser Ala Val Gly Val Leu Tyr Pro Pro
368 65 70 75 80
371 His Leu Val Tyr Lys Ile Lys Ser Ile Cys Ile Leu Ser Ala Asp Asp
372 85 90 95
375 Pro Asp Thr Asp Leu Pro Asn Cys Thr Lys His Thr Lys Ser Asn Gln
376 100 105 110
379 Ser Thr Pro Thr His Ser Val Ser Thr Ser Asn Asn Asn Asn Ala Ser
380 115 120 125
383 Val Pro Ser Ser Gly Gly Ser Ser Lys Ser Thr Lys Leu Phe Glu
384 130 135 140
387 Gly Met Asn Lys Thr Trp Gly Ala Val Lys Ser Ala Gly Asn Thr Ile
388 145 150 155 160
391 Lys Asn Thr Thr Gln Gln Ala Ala Asn Leu Ala Thr Lys Gln Val Lys
392 165 170 175
395 Ser Ser Val Gly Ile Arg Glu Pro Arg His Ile Glu Arg Arg Ile Thr
396 180 185 190
399 Glu Glu Leu His Lys Ile Phe Asp Glu Thr Asp Ser Phe Tyr Phe Ser
400 195 200 205
403 Phe Asp Cys Asp Ile Thr Asn Asn Leu Gln Arg His Glu Ala Lys Ser
404 210 215 220

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date